

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/913,756

ENTERED

CRF Processing Date: 3/9/2002

Edited by: AK

Verified by: AK (STIC staff)

09/09 #24

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☒ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: 12
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☒ Other: Seq 16 corrected amino acid nos:

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



PCT09

RAW SEQUENCE LISTING

DATE: 03/07/2002

PATENT APPLICATION: US/09/913,756

TIME: 18:40:43

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\03072002\I913756.raw

3 <110> APPLICANT: Chiari, Rita
 4 Coulie, Pierre
 5 Boon-Falleur, Thierry
 7 <120> TITLE OF INVENTION: TYROSINE KINASE RECEPTOR EphA3 ANTIGENIC PEPTIDES
 9 <130> FILE REFERENCE: L0461/7121
 11 <140> CURRENT APPLICATION NUMBER: US 09/913,756
 12 <141> CURRENT FILING DATE: 2000-02-18
 14 <150> PRIOR APPLICATION NUMBER: US 60/121,170
 15 <151> PRIOR FILING DATE: 1999-02-22
 17 <150> PRIOR APPLICATION NUMBER: US 60/158,566
 18 <151> PRIOR FILING DATE: 1999-10-08
 20 <160> NUMBER OF SEQ ID NOS: 63
 22 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 43
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Artificial sequence
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 31 <221> NAME/KEY: primer_bind
 32 <222> LOCATION: 1..43
 33 <223> OTHER INFORMATION: synthetic oligo(dT) primer
 35 <220> FEATURE:
 36 <221> NAME/KEY: unsure
 37 <222> LOCATION: 43..43
 38 <223> OTHER INFORMATION: n = a, c, g or t
 40 <400> SEQUENCE: 1
 41 **W** > ataagaatgc ggccgctaaa ctattttttt tttttttttt tvn' 43
 44 <210> SEQ ID NO: 2
 45 <211> LENGTH: 3149
 46 <212> TYPE: DNA
 47 <213> ORGANISM: Homo sapiens
 49 <220> FEATURE:
 50 <221> NAME/KEY: CDS
 51 <222> LOCATION: 101..3052
 53 <400> SEQUENCE: 2
 54 ccatggatgg taacttctcc agcaatcaga gcgctccccc tcacatcagt ggcattgttc 60
 55 atggagatat gctcctctca ctgccctctg caccagcaac atg gat tgt cag ctc 115
 56 Met Asp Cys Gln Leu
 57 1 5
 59 tcc atc ctc ctc ctt ctc agc tgc tct gtt ctc gac agc ttc ggg gaa 163
 60 Ser Ile Leu Leu Leu Leu Ser Cys Ser Val Leu Asp Ser Phe Gly Glu
 61 10 15 20
 63 ctg att ccg cag cct tcc aat gaa gtc aat cta ctg gat tca aaa aca 211

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64	Leu Ile Pro Gln Pro Ser Asn Glu Val Asn Leu Leu Asp Ser Lys Thr	
65	25 30 35	
67	att caa ggg gag ctg ggc tgg atc tct tat cca tca cat ggg tgg gaa	259
68	Ile Gln Gly Glu Leu Gly Trp Ile Ser Tyr Pro Ser His Gly Trp Glu	
69	40 45 50	
71	gag atc agt ggt gtg gat gaa cat tac aca ccc atc agg act tac cag	307
72	Glu Ile Ser Gly Val Asp Glu His Tyr Thr Pro Ile Arg Thr Tyr Gln	
73	55 60 65	
75	gtg tgc aat gtc atg gac cac agt caa aac aat tgg ctg aga aca aac	355
76	Val Cys Asn Val Met Asp His Ser Gln Asn Asn Trp Leu Arg Thr Asn	
77	70 75 80 85	
79	tgg gtc ccc agg aac tca gct cag aag att tat gtg gag ctc aag ttc	403
80	Trp Val Pro Arg Asn Ser Ala Gln Lys Ile Tyr Val Glu Leu Lys Phe	
81	90 95 100	
83	act cta cga gac tgc aat agc att cca ttg gtt tta gga act tgc aag	451
84	Thr Leu Arg Asp Cys Asn Ser Ile Pro Leu Val Leu Gly Thr Cys Lys	
85	105 110 115	
87	gag aca ttc aac ctg tac tac atg gag tct gat gat gat cat ggg gtg	499
88	Glu Thr Phe Asn Leu Tyr Tyr Met Glu Ser Asp Asp Asp His Gly Val	
89	120 125 130	
91	aaa ttt cga gag cat cag ttt aca aag att gac acc att gca gct gat	547
92	Lys Phe Arg Glu His Gln Phe Thr Lys Ile Asp Thr Ile Ala Ala Asp	
93	135 140 145	
95	gaa agt ttc act caa atg gat ctt ggg gac cgt att ctg aag ctc aac	595
96	Glu Ser Phe Thr Gln Met Asp Leu Gly Asp Arg Ile Leu Lys Leu Asn	
97	150 155 160 165	
99	act gag att aga gaa gta ggt cct gtc aac aag aag gga ttt tat ttg	643
100	Thr Glu Ile Arg Glu Val Gly Pro Val Asn Lys Lys Gly Phe Tyr Leu	
101	170 175 180	
103	gca ttt caa gat gtt ggt gct tgt gtt gcc ttg gtg tct gtg aga gta	691
104	Ala Phe Gln Asp Val Gly Ala Cys Val Ala Leu Val Ser Val Arg Val	
105	185 190 195	
107	tac ttc aaa aag tgc cca ttt aca gtg aag aat ctg gct atg ttt cca	739
108	Tyr Phe Lys Lys Cys Pro Phe Thr Val Lys Asn Leu Ala Met Phe Pro	
109	200 205 210	
111	gac acg gta ccc atg gac tcc cag tcc ctg gtg gag gtt aga ggg tct	787
112	Asp Thr Val Pro Met Asp Ser Gln Ser Leu Val Glu Val Arg Gly Ser	
113	215 220 225	
115	tgt gtc aac aat tct aag gag gaa gat cct cca agg atg tac tgc agt	835
116	Cys Val Asn Asn Ser Lys Glu Glu Asp Pro Pro Arg Met Tyr Cys Ser	
117	230 235 240 245	
119	aca gaa ggc gaa tgg ctt gta ccc att ggc aag tgt tcc tgc aat gct	883
120	Thr Glu Gly Glu Trp Leu Val Pro Ile Gly Lys Cys Ser Cys Asn Ala	
121	250 255 260	
123	ggc tat gaa gaa aga ggt ttt atg tgc caa gct tgt cga cca ggt ttc	931
124	Gly Tyr Glu Glu Arg Gly Phe Met Cys Gln Ala Cys Arg Pro Gly Phe	
125	265 270 275	
127	tac aag gca ttg gat ggt aat atg aag tgt gct aag tgc ccg cct cac	979
128	Tyr Lys Ala Leu Asp Gly Asn Met Lys Cys Ala Lys Cys Pro Pro His	

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129				280				285				290						
131	agt	tct	act	cag	gaa	gat	ggt	tca	atg	aac	tgc	agg	tgt	gag	aat	aat		1027
132	Ser	Ser	Thr	Gln	Glu	Asp	Gly	Ser	Met	Asn	Cys	Arg	Cys	Glu	Asn	Asn		
133				295			300					305						
135	tac	ttc	cgg	gca	gac	aaa	gac	cct	cca	tcc	atg	gct	tgt	acc	cga	cct		1075
136	Tyr	Phe	Arg	Ala	Asp	Lys	Asp	Pro	Pro	Ser	Met	Ala	Cys	Thr	Arg	Pro		
137	310					315					320					325		
139	cca	tct	tca	cca	aga	aat	gtt	atc	tct	aat	ata	aac	gag	acc	tca	gtt		1123
140	Pro	Ser	Ser	Pro	Arg	Asn	Val	Ile	Ser	Asn	Ile	Asn	Glu	Thr	Ser	Val		
141					330					335					340			
143	atc	ctg	gac	tgg	agt	tgg	ccc	ctg	gac	aca	gga	ggc	cgg	aaa	gat	gtt		1171
144	Ile	Leu	Asp	Trp	Ser	Trp	Pro	Leu	Asp	Thr	Gly	Gly	Arg	Lys	Asp	Val		
145				345					350					355				
147	acc	ttc	aac	atc	ata	tgt	aaa	aaa	tgt	ggg	tgg	aat	ata	aaa	cag	tgt		1219
148	Thr	Phe	Asn	Ile	Ile	Cys	Lys	Lys	Cys	Gly	Trp	Asn	Ile	Lys	Gln	Cys		
149			360				365					370						
151	gag	cca	tgc	agc	cca	aat	gtc	cgc	ttc	ctc	cct	cga	cag	ttt	gga	ctc		1267
152	Glu	Pro	Cys	Ser	Pro	Asn	Val	Arg	Phe	Leu	Pro	Arg	Gln	Phe	Gly	Leu		
153			375				380					385						
155	acc	aac	acc	acg	gtg	aca	gtg	aca	gac	ctt	ctg	gca	cat	act	aac	tac		1315
156	Thr	Asn	Thr	Thr	Val	Thr	Val	Thr	Asp	Leu	Leu	Ala	His	Thr	Asn	Tyr		
157	390					395					400					405		
159	acc	ttt	gag	att	gat	gcc	gtt	aat	ggg	gtg	tca	gag	ctg	agc	tcc	cca		1363
160	Thr	Phe	Glu	Ile	Asp	Ala	Val	Asn	Gly	Val	Ser	Glu	Leu	Ser	Ser	Pro		
161				410					415						420			
163	cca	aga	cag	ttt	gct	gcg	gtc	agc	atc	aca	act	aat	cag	gct	gct	cca		1411
164	Pro	Arg	Gln	Phe	Ala	Ala	Val	Ser	Ile	Thr	Thr	Asn	Gln	Ala	Ala	Pro		
165			425					430					435					
167	tca	cct	gtc	ctg	acg	att	aag	aaa	gat	cgg	acc	tcc	aga	aat	agc	atc		1459
168	Ser	Pro	Val	Leu	Thr	Ile	Lys	Lys	Asp	Arg	Thr	Ser	Arg	Asn	Ser	Ile		
169			440				445						450					
171	tct	ttg	tcc	tgg	caa	gaa	cct	gaa	cat	cct	aat	ggg	atc	ata	ttg	gac		1507
172	Ser	Leu	Ser	Trp	Gln	Glu	Pro	Glu	His	Pro	Asn	Gly	Ile	Ile	Leu	Asp		
173			455				460					465						
175	tac	gag	gtc	aaa	tac	tat	gaa	aag	cag	gaa	caa	gaa	aca	agt	tat	acc		1555
176	Tyr	Glu	Val	Lys	Tyr	Tyr	Glu	Lys	Gln	Glu	Gln	Glu	Thr</					

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195	gca gta gca att att ctc ctc act gtt gtc atc tat gtt ttg att ggg	1795
196	Ala Val Ala Ile Ile Leu Leu Thr Val Val Ile Tyr Val Leu Ile Gly	
197	550 555 560 565	
199	agg ttc tgt ggc tat aag tca aaa cat ggg gca gat gaa aaa aga ctt	1843
200	Arg Phe Cys Gly Tyr Lys Ser Lys His Gly Ala Asp Glu Lys Arg Leu	
201	570 575 580	
203	cat ttt ggc aat ggg cat tta aaa ctt cca ggt ctc agg act tat gtt	1891
204	His Phe Gly Asn Gly His Leu Lys Leu Pro Gly Leu Arg Thr Tyr Val	
205	585 590 595	
207	gac cca cat aca tat gaa gac cct acc caa gct gtt cat gag ttt gcc	1939
208	Asp Pro His Thr Tyr Glu Asp Pro Thr Gln Ala Val His Glu Phe Ala	
209	600 605 610	
211	aag gaa ttg gat gcc acc aac ata tcc att gat aaa gtt gtt gga gca	1987
212	Lys Glu Leu Asp Ala Thr Asn Ile Ser Ile Asp Lys Val Val Gly Ala	
213	615 620 625	
215	ggt gaa ttt gga gag gtg tgc agt ggt cgc tta aaa ctt cct tca aaa	2035
216	Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu Lys Leu Pro Ser Lys	
217	630 635 640 645	
219	aaa gag att tca gtg gcc att aaa acc ctg aaa gtt ggc tac aca gaa	2083
220	Lys Glu Ile Ser Val Ala Ile Lys Thr Leu Lys Val Gly Tyr Thr Glu	
221	650 655 660	
223	aag cag agg aga gac ttc ctg gga gaa gca agc att atg gga cag ttt	2131
224	Lys Gln Arg Arg Asp Phe Leu Gly Glu Ala Ser Ile Met Gly Gln Phe	
225	665 670 675	
227	gac cac ccc aat atc att cga ctg gaa gga gtt gtt acc aaa agt aag	2179
228	Asp His Pro Asn Ile Ile Arg Leu Glu Gly Val Val Thr Lys Ser Lys	
229	680 685 690	
231	cca gtt atg att gtc aca gaa tac atg gag aat ggt tcc ttg gat agt	2227
232	Pro Val Met Ile Val Thr Glu Tyr Met Glu Asn Gly Ser Leu Asp Ser	
233	695 700 705	
235	ttc cta cgt aaa cac gat gcc cag ttt act gtc att cag cta gtg ggg	2275
236	Phe Leu Arg Lys His Asp Ala Gln Phe Thr Val Ile Gln Leu Val Gly	
237	710 715 720 725	
239	atg ctt cga ggg ata gca tct ggc atg aag tac ctg tca gac atg ggc	2323
240	Met Leu Arg Gly Ile Ala Ser Gly Met Lys Tyr Leu Ser Asp Met Gly	
241	730 735 740	
243	tat gtt cac cga gac ctc gct gct cgg aac atc ttg atc aac agt aac	2371
244	Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Ile Asn Ser Asn	
245	745 750 755	
247	ttg gtg tgt aag gtt tct gat ttc gga ctt tcg cgt gtc ctg gag gat	2419
248	Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp	
249	760 765 770	
251	gac cca gaa gct gct tat aca aca aga gga ggg aag atc cca atc agg	2467
252	Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly Lys Ile Pro Ile Arg	
253	775 780 785	
255	tgg aca tca cca gaa gct ata gcc tac cgc aag ttc acg tca gcc agc	2515
256	Trp Thr Ser Pro Glu Ala Ile Ala Tyr Arg Lys Phe Thr Ser Ala Ser	
257	790 795 800 805	
259	gat gta tgg agt tat ggg att gtt ctc tgg gag gtg atg tct tat gga	2563

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Output Set: N:\CRF3\03072002\I913756.raw

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260 Asp Val Trp Ser Tyr Gly Ile Val Leu Trp Glu Val Met Ser Tyr Gly
261      810      815      820
263 gag aga cca tac tgg gag atg tcc aat cag gat gta att aaa gct gta 2611
264 Glu Arg Pro Tyr Trp Glu Met Ser Asn Gln Asp Val Ile Lys Ala Val
265      825      830      835
267 gat gag ggc tat cga ctg cca ccc ccc atg gac tgc cca gct gcc ttg 2659
268 Asp Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp Cys Pro Ala Ala Leu
269      840      845      850
271 tat cag ctg atg ctg gac tgc tgg cag aaa gac agg aac aac aga ccc 2707
272 Tyr Gln Leu Met Leu Asp Cys Trp Gln Lys Asp Arg Asn Asn Arg Pro
273      855      860      865
275 aag ttt gag cag att gtt agt att ctg gac aag ctt atc cgg aat ccc 2755
276 Lys Phe Glu Gln Ile Val Ser Ile Leu Asp Lys Leu Ile Arg Asn Pro
277 870      875      880      885
279 ggc agc ctg aag atc atc acc agt gca gcc gca agg cca tca aac ctt 2803
280 Gly Ser Leu Lys Ile Ile Thr Ser Ala Ala Ala Arg Pro Ser Asn Leu
281      890      895      900
283 ctt ctg gac caa agc aat gtg gat atc tct acc ttc cgc aca aca ggt 2851
284 Leu Leu Asp Gln Ser Asn Val Asp Ile Ser Thr Phe Arg Thr Thr Gly
285      905      910      915
287 gac tgg ctt aat ggt gtc cgg aca gca cac tgc aag gaa atc ttc acg 2899
288 Asp Trp Leu Asn Gly Val Arg Thr Ala His Cys Lys Glu Ile Phe Thr
289      920      925      930
291 ggc gtg gag tac agt tct tgt gac aca ata gcc aag att tcc aca gat 2947
292 Gly Val Glu Tyr Ser Ser Cys Asp Thr Ile Ala Lys Ile Ser Thr Asp
293      935      940      945
295 gac atg aaa aag gtt ggt gtc acc gtg gtt ggg cca cag aag aag atc 2995
296 Asp Met Lys Lys Val Gly Val Thr Val Val Gly Pro Gln Lys Lys Ile
297 950      955      960      965
299 atc agt agc att aaa gct cta gaa acg caa tca aag aat ggc cca gtt 3043
300 Ile Ser Ser Ile Lys Ala Leu Glu Thr Gln Ser Lys Asn Gly Pro Val
301      970      975      980
303 ccc gtg taa agcagcagcg aagtgttct ggacggaagt ggtggctgtg 3092
304 Pro Val
307 gaaggcgtca agtcatactg cagacagaca ataattctgg agatactggt ggaagtt 3149
309 <210> SEQ ID NO: 3
310 <211> LENGTH: 983
311 <212> TYPE: PRT
312 <213> ORGANISM: Homo sapiens
314 <400> SEQUENCE: 3
315 Met Asp Cys Gln Leu Ser Ile Leu Leu Leu Leu Ser Cys Ser Val Leu
316 1 5 10 15
317 Asp Ser Phe Gly Glu Leu Ile Pro Gln Pro Ser Asn Glu Val Asn Leu
318 20 25 30
319 Leu Asp Ser Lys Thr Ile Gln Gly Glu Leu Gly Trp Ile Ser Tyr Pro
320 35 40 45
321 Ser His Gly Trp Glu Glu Ile Ser Gly Val Asp Glu His Tyr Thr Pro
322 50 55 60
323 Ile Arg Thr Tyr Gln Val Cys Asn Val Met Asp His Ser Gln Asn Asn

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/913,756

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 43